SEQUENCE LISTING

<110> Prayaga, Suhhirdas K
Shimkets, Richard A

<120> Novel Polypeptides and Polynucleotides Encoding Same

<130> 15966-615

<140> 09/732,436
<141> 2000-12-07

<150> 60/169,887
<151> 1999-12-09

<150> 60/170,230
<151> 1999-12-10

<160> 27

<170> PatentIn Ver. 2.1

<210> 1
<211> 475
<212> DNA
<213> Homo sapiens

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cagcctcttt ttacacaagg gcttgtctga tgcttggaat agggccttcc tggacaaact 180
ccagactgga tttcatcagc agctggaaga cctggagacc tgctttggta tagaggatgg 240
gaagcaagag tctgccctgg aaattgaggg ccctacactg gccataaaga ggtacttcca 300
gggagtacat ttcttcttga aagagaggaa attcaggaac tgtacctggg aggttgtcgt 360
aatggtaaag ggatttttct taagcacaaa acttcaagaa aaagagaaca gaagaaaaga 420
gaactgcaaa aaaaatctgg aaaaggtaat ctatttagca gaagagtgaa agctg 475

<210> 2
<211> 154
<212> PRT
<213> Homo sapiens

<400> 2
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1 5 10 15

Ser Leu Phe Cys Asp Leu Pro Lys Ala Gln Val Ile Ser Ala Leu His
20 25 30

Lys Met His Gln Gln Ile Phe Ser Leu Phe Leu His Lys Gly Leu Ser
35 40 45

Asp Ala Trp Asn Arg Ala Phe Leu Asp Lys Leu Gln Thr Gly Phe His
50 55 60

Gln Gln Leu Glu Asp Leu Glu Thr Cys Phe Gly Ile Glu Asp Gly Lys

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 65                  70                  75                  80

Gln Glu Ser Ala Leu Glu Ile Glu Gly Pro Thr Leu Ala Ile Lys Arg
                85                  90                  95

Tyr Phe Gln Gly Val His Phe Phe Leu Lys Glu Arg Lys Phe Arg Asn
            100                 105                 110

Cys Thr Trp Glu Val Val Val Met Val Lys Gly Phe Phe Leu Ser Thr
        115                 120                 125

Lys Leu Gln Glu Lys Glu Asn Arg Arg Lys Glu Asn Cys Lys Lys Asn
    130                 135                 140

Leu Glu Lys Val Ile Tyr Leu Ala Glu Glu
145                 150
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<210> 3
<211> 610
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (74)..(208)
<223> Wherein n is a or t or c or g.

<400> 3
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nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 180
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cttcctggac aaactccaga ctggatttca tcagcagctg gaagacctgg agacctgctt 360
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aaagaggtac ttccagggag tacatttctt cttgaaagag aggaaattca ggaactgtac 480
ctgggaggtt gtcgtaatgg taaagggatt tttcttaagc acaaaacttc aagaaaaaga 540
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gtgaaagctg   610

D5 cont

<210> 4
<211> 199
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (24)..(68)
<223> Wherein Xaa is any amino acid.

<400> 4
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  1   5   10   15

Ser Leu Phe Cys Asp Leu Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

```
            20                  25                  30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
         35                  40                  45

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
     50                  55                  60

Xaa Xaa Xaa Xaa Lys Ala Gln Val Ile Ser Ala Leu His Lys Met His
 65                  70                  75                  80

Gln Gln Ile Phe Ser Leu Phe Leu His Lys Gly Leu Ser Asp Ala Trp
                 85                  90                  95

Asn Arg Ala Phe Leu Asp Lys Leu Gln Thr Gly Phe His Gln Gln Leu
            100                 105                 110

Glu Asp Leu Glu Thr Cys Phe Gly Ile Glu Asp Gly Lys Gln Glu Ser
        115                 120                 125

Ala Leu Glu Ile Glu Gly Pro Thr Leu Ala Ile Lys Arg Tyr Phe Gln
    130                 135                 140

Gly Val His Phe Phe Leu Lys Glu Arg Lys Phe Arg Asn Cys Thr Trp
145                 150                 155                 160

Glu Val Val Val Met Val Lys Gly Phe Phe Leu Ser Thr Lys Leu Gln
                165                 170                 175

Glu Lys Glu Asn Arg Arg Lys Glu Asn Cys Lys Lys Asn Leu Glu Lys
            180                 185                 190

Val Ile Tyr Leu Ala Glu Glu
        195
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<210> 5
<211> 1887
<212> DNA
<213> Homo sapiens

<400> 5
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gcagccgagc tgcggctggc agacaacttc atcgcctccg tgcgccgccg cgacctggcc 240
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ggcgccttcg ccgacctgcg ggccctgcgt gccctgcacc tggatggcaa ccggctgacc 360
tcactgggcg agggccagct gcgcggcctg gtcaacttgc gccacctcat cctcagcaac 420
aaccagctgg cagcgctggc ggccggcgcc ctggatgatt gtgccgagac actggaggac 480
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tcccgcctgc acaagctggc ccggctggac atgacctcca accgcctgac cacaatccca 660
cccgacccac tcttctcccg cctgcccctg ctcgccaggc cccggggctc gcccgcctct 720
gccctggtgc tggcctttgg cgggaacccc ctgcactgca actgcgagct ggtgtggctg 780
cgtcgcctgg cgcgggagga cgacctcgag gcctgcgcgt ccccacctgc tctgggcggc 840
cgctacttct gggcggtggg cgaggaggag tttgtctgcg agccgcccgt ggtgactcac 900

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agccgtgccc gcgccttccc caatgggacg ctggagctgc tggtcaccga gccgggtgat 1080
ggtggcatct tcacctgcat tgcggccaat gcagctggcg aggccacagc tgctgtggag 1140
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cgggacgggg atcctgatgc tctcacccca ccctccgctg cctctgcttc tgccaaggtg 1260
gccgacactg ggcccccctac cgaccgtggc gtccaggtga ctgagcacgg ggccacagct 1320
gctcttgtcc agtggccgga tcagcggcct atcccgggca tccgcatgta ccagatccag 1380
tacaacagct cggctgatga catcctcgtc tacaggatga tcccggcgga gagccgctcg 1440
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gaggacagcg ccacggggct cacggccacg cggcctgtgg gctgcgcccg cttctccacc 1560
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atcgcgctgg gcggcgtcat cgtagcctcg gtactggtct tcatcttcgt gctgctaatg 1680
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cccggccacg aacctgtggg accctag                                     1887
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<210> 6
<211> 628
<212> PRT
<213> Homo sapiens

<400> 6

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Met Ala Ile Leu Pro Leu Leu Leu Cys Leu Leu Pro Leu Ala Pro Ala
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Ser Ser Pro Pro Gln Ser Ala Thr Pro Ser Pro Cys Pro Arg Arg Cys
             20                  25                  30

Arg Cys Gln Thr Gln Ser Leu Pro Leu Ser Val Leu Cys Pro Gly Ala
         35                  40                  45

Gly Leu Leu Phe Val Pro Pro Ser Leu Asp Arg Arg Ala Ala Glu Leu
     50                  55                  60

Arg Leu Ala Asp Asn Phe Ile Ala Ser Val Arg Arg Arg Asp Leu Ala
 65                  70                  75                  80

Asn Met Thr Gly Leu Leu His Leu Ser Leu Ser Arg Asn Thr Ile Arg
                 85                  90                  95

His Val Ala Ala Gly Ala Phe Ala Asp Leu Arg Ala Leu Arg Ala Leu
            100                 105                 110

His Leu Asp Gly Asn Arg Leu Thr Ser Leu Gly Glu Gly Gln Leu Arg
        115                 120                 125

Gly Leu Val Asn Leu Arg His Leu Ile Leu Ser Asn Asn Gln Leu Ala
    130                 135                 140

Ala Leu Ala Ala Gly Ala Leu Asp Asp Cys Ala Glu Thr Leu Glu Asp
145                 150                 155                 160

Leu Asp Leu Ser Tyr Asn Asn Leu Glu Gln Leu Pro Trp Glu Ala Leu
                165                 170                 175
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D5 Cont

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Gly Arg Leu Gly Asn Val Asn Thr Leu Gly Leu Asp His Asn Leu Leu
            180                 185                 190

Ala Ser Val Pro Ala Gly Ala Phe Ser Arg Leu His Lys Leu Ala Arg
        195                 200                 205

Leu Asp Met Thr Ser Asn Arg Leu Thr Thr Ile Pro Pro Asp Pro Leu
    210                 215                 220

Phe Ser Arg Leu Pro Leu Leu Ala Arg Pro Arg Gly Ser Pro Ala Ser
225                 230                 235                 240

Ala Leu Val Leu Ala Phe Gly Gly Asn Pro Leu His Cys Asn Cys Glu
                245                 250                 255

Leu Val Trp Leu Arg Arg Leu Ala Arg Glu Asp Asp Leu Glu Ala Cys
            260                 265                 270

Ala Ser Pro Pro Ala Leu Gly Gly Arg Tyr Phe Trp Ala Val Gly Glu
        275                 280                 285

Glu Glu Phe Val Cys Glu Pro Pro Val Val Thr His Arg Ser Pro Pro
    290                 295                 300

Leu Ala Val Pro Ala Gly Arg Pro Ala Ala Leu Arg Cys Arg Ala Val
305                 310                 315                 320

Gly Asp Pro Glu Pro Arg Val Arg Trp Val Ser Pro Gln Gly Arg Leu
                325                 330                 335

Leu Gly Asn Ser Ser Arg Ala Arg Ala Phe Pro Asn Gly Thr Leu Glu
            340                 345                 350

Leu Leu Val Thr Glu Pro Gly Asp Gly Gly Ile Phe Thr Cys Ile Ala
        355                 360                 365

Ala Asn Ala Ala Gly Glu Ala Thr Ala Ala Val Glu Leu Thr Val Gly
    370                 375                 380

Pro Pro Pro Pro Pro Gln Leu Ala Asn Ser Thr Ser Cys Asp Pro Pro
385                 390                 395                 400

Arg Asp Gly Asp Pro Asp Ala Leu Thr Pro Pro Ser Ala Ala Ser Ala
                405                 410                 415

Ser Ala Lys Val Ala Asp Thr Gly Pro Pro Thr Asp Arg Gly Val Gln
            420                 425                 430

Val Thr Glu His Gly Ala Thr Ala Ala Leu Val Gln Trp Pro Asp Gln
        435                 440                 445

Arg Pro Ile Pro Gly Ile Arg Met Tyr Gln Ile Gln Tyr Asn Ser Ser
    450                 455                 460

Ala Asp Asp Ile Leu Val Tyr Arg Met Ile Pro Ala Glu Ser Arg Ser
465                 470                 475                 480
```

D5 Cont

```
Phe Leu Leu Thr Asp Leu Ala Ser Gly Arg Thr Tyr Asp Leu Cys Val
                485                 490                 495

Leu Ala Val Tyr Glu Asp Ser Ala Thr Gly Leu Thr Ala Thr Arg Pro
            500                 505                 510

Val Gly Cys Ala Arg Phe Ser Thr Glu Pro Ala Leu Arg Pro Cys Gly
        515                 520                 525

Ala Pro His Ala Pro Phe Leu Gly Gly Thr Met Ile Ile Ala Leu Gly
    530                 535                 540

Gly Val Ile Val Ala Ser Val Leu Val Phe Ile Phe Val Leu Leu Met
545                 550                 555                 560

Arg Tyr Lys Val His Gly Gly Gln Pro Pro Gly Lys Ala Lys Ile Pro
                565                 570                 575

Ala Pro Val Ser Ser Val Cys Ser Gln Thr Asn Gly Ala Leu Gly Pro
            580                 585                 590

Thr Pro Thr Pro Ala Pro Pro Ala Pro Glu Pro Ala Ala Leu Arg Ala
        595                 600                 605

His Thr Val Val Gln Leu Asp Cys Glu Pro Trp Gly Pro Gly His Glu
    610                 615                 620

Pro Val Gly Pro
625
```

<210> 7
<211> 802
<212> DNA
<213> Equus caballus

<400> 7

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ttttccccat ggccctcctg ccctctctct tgacggccct ggtggtgtac gagttatggc 180
cctgtggagc tctgggctgt gacctgcctc agaaccacat cctggttagc aggaagaact 240
tcgtgcttct gggccaaatg agcagaatct cctccgcaat ctgtctgaag gacagaaaag 300
acttcaggtt cccccaggac atggcggatg gcaggcagtt cccagaggcc caggccgcgt 360
ctgtcctcca cgagatgctc cagcagatct tcagcctctt ccacacagag cgctcgtctg 420
ctgcctggaa cacgaccctc ctggacgaac tctgcacggg actccttcgg cagctggaag 480
acctggacac ctgtttggag caggagatgg gagaggaaga atctgccctg ggaactgtgc 540
gccctacact ggccgtgaag aggtacttcc gggggatcca tctctacctg aaagagaaga 600
aatacagtga ctgtgcctgg gagattgtcc gaatggaaat catgagatcc ttctcttcat 660
cagcaaacct gcaaggaagg ttaagaatga aggatggaga cctgggctca ccttgaaatg 720
attctcctta actactgggt catgttaccc ttgcatatgt ccttggtcat ttcaaaaggc 780
tcttatttct gctttagtct ag                                        802
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<210> 8
<211> 195
<212> PRT

<213> Homo sapiens

<400> 8

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Met Ala Leu Leu Phe Pro Leu Leu Ala Ala Leu Val Met Thr Ser Tyr
  1               5                  10                  15

Ser Pro Val Gly Ser Leu Gly Cys Asp Leu Pro Gln Asn His Gly Leu
             20                  25                  30

Leu Ser Arg Asn Thr Leu Val Leu Leu His Gln Met Arg Arg Ile Ser
         35                  40                  45

Pro Phe Leu Cys Leu Lys Asp Arg Arg Asp Phe Arg Phe Pro Gln Glu
     50                  55                  60

Met Val Lys Gly Ser Gln Leu Gln Lys Ala His Val Met Ser Val Leu
 65                  70                  75                  80

His Glu Met Leu Gln Gln Ile Phe Ser Leu Phe His Thr Glu Arg Ser
                 85                  90                  95

Ser Ala Ala Trp Asn Met Thr Leu Leu Asp Gln Leu His Thr Gly Leu
            100                 105                 110

His Gln Gln Leu Gln His Leu Glu Thr Cys Leu Leu Gln Val Val Gly
        115                 120                 125

Glu Gly Glu Ser Ala Gly Ala Ile Ser Ser Pro Ala Leu Thr Leu Arg
    130                 135                 140

Arg Tyr Phe Gln Gly Ile Arg Val Tyr Leu Lys Glu Lys Lys Tyr Ser
145                 150                 155                 160

Asp Cys Ala Trp Glu Val Val Arg Met Glu Ile Met Lys Ser Leu Phe
                165                 170                 175

Leu Ser Thr Asn Met Gln Glu Arg Leu Arg Ser Lys Asp Arg Asp Leu
            180                 185                 190

Gly Ser Ser
        195
```

D5 Cont

<210> 9
<211> 195
<212> PRT
<213> Equus caballus

<400> 9

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Met Ala Phe Ser Val Ser Ser Leu Met Ala Leu Val Val Ile Ser Ser
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Ser Pro Val Ser Ser Met Ser Cys Asp Leu Pro Ala Ser Leu Asp Leu
             20                  25                  30

Arg Lys Gln Glu Thr Leu Arg Val Leu His Gln Met Glu Thr Ile Ser
         35                  40                  45
```

```
Pro Pro Ser Cys Leu Lys His Arg Thr Asp Phe Arg Phe Pro Gln Glu
     50                  55                  60

Gln Leu Asp Gly Arg Gln Phe Pro Glu Ala Gln Ala Thr Ser Val Leu
 65                  70                  75                  80

Gln Glu Met Leu Gln Gln Ile Val Ser Leu Phe His Thr Glu Arg Ser
                 85                  90                  95

Ser Ala Ala Trp Asn Thr Thr Leu Leu Asp Arg Leu Leu Ala Gly Leu
            100                 105                 110

His Gln Gln Leu Glu Asp Leu Asn Thr Cys Leu Asp Glu Gln Thr Gly
        115                 120                 125

Glu Glu Glu Ser Ala Leu Gly Thr Val Gly Pro Thr Leu Ala Val Lys
    130                 135                 140

Arg Tyr Phe Arg Arg Ile Arg Leu Tyr Leu Thr Glu Lys Lys Tyr Ser
145                 150                 155                 160

Asp Cys Ala Trp Glu Ile Val Arg Val Asp Ile Met Arg Ser Phe Ser
                165                 170                 175

Ser Ser Ala Asn Leu Gln Gly Arg Leu Gly Met Lys Asp Gly Asp Leu
            180                 185                 190

Gly Ser Pro
        195
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<210> 10
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:pfam00143
Domain 71-187

D5 Cont

<400> 10

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  1               5                  10                  15

Ile Phe His Phe Phe Cys Thr Glu Ala Ser Ser Ser Ala Ala Trp Asn
             20                  25                  30

Thr Thr Leu Leu Glu Glu Phe Cys Thr Gly Leu Asp Arg Gln Leu Thr
         35                  40                  45

Arg Leu Glu Ala Cys Val Leu Gln Glu Val Glu Glu Gly Glu Ala Pro
     50                  55                  60

Leu Thr Asn Glu Asp Ile His Pro Glu Asp Ser Ile Leu Arg Asn Tyr
 65                  70                  75                  80
```

```
Phe Gln Arg Leu Ser Leu Tyr Leu Gln Glu Lys Lys Tyr Ser Pro Cys
                85                  90                  95

Ala Trp Glu Ile Val Arg Ala Glu Ile Met Arg Ser Leu Tyr Tyr Ser
            100                 105                 110

Ser Thr Ala Leu Gln
        115
```

<210> 11
<211> 194
<212> PRT
<213> Felis catus

<400> 11

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Met Ala Leu Pro Ser Ser Phe Leu Val Ala Leu Val Ala Leu Gly Cys
  1               5                  10                  15

Asn Ser Val Cys Ser Leu Gly Cys Asp Leu Pro Gln Thr His Gly Leu
             20                  25                  30

Leu Asn Arg Arg Ala Leu Thr Leu Leu Gly Gln Met Arg Arg Leu Pro
         35                  40                  45

Ala Ser Ser Cys Gln Lys Asp Arg Asn Asp Phe Ala Phe Pro Gln Asp
     50                  55                  60

Val Phe Gly Gly Asp Gln Ser His Lys Ala Gln Ala Leu Ser Val Val
 65                  70                  75                  80

His Val Thr Asn Gln Lys Ile Phe His Phe Phe Cys Thr Glu Ala Ser
                85                  90                  95

Ser Ser Ala Ala Trp Asn Thr Thr Leu Leu Glu Glu Phe Cys Thr Gly
            100                 105                 110

Leu Asp Arg Gln Leu Thr Arg Leu Glu Ala Cys Val Leu Gln Glu Val
        115                 120                 125

Glu Glu Gly Glu Ala Pro Leu Thr Asn Glu Asp Ile His Pro Glu Asp
    130                 135                 140

Ser Ile Leu Arg Asn Tyr Phe Gln Arg Leu Ser Leu Tyr Leu Gln Glu
145                 150                 155                 160

Lys Lys Tyr Ser Pro Cys Ala Trp Glu Ile Val Arg Ala Glu Ile Met
                165                 170                 175

Arg Ser Leu Tyr Tyr Ser Ser Thr Ala Leu Gln Lys Arg Leu Arg Ser
            180                 185                 190

Glu Lys
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<210> 12

<211> 195
<212> PRT
<213> Homo sapiens

<400> 12
Met Ala Phe Val Leu Ser Leu Leu Met Ala Leu Val Leu Val Ser Tyr
1 5 10 15

Gly Pro Gly Gly Ser Leu Gly Cys Asp Leu Ser Gln Asn His Val Leu
20 25 30

Val Gly Arg Lys Asn Leu Arg Leu Leu Asp Glu Met Arg Arg Leu Ser
35 40 45

Pro His Phe Cys Leu Gln Asp Arg Lys Asp Phe Ala Leu Pro Gln Glu
50 55 60

Met Val Glu Gly Gly Gln Leu Gln Glu Ala Gln Ala Ile Ser Val Leu
65 70 75 80

His Glu Met Leu Gln Gln Ser Phe Asn Leu Phe His Thr Glu His Ser
85 90 95

Ser Ala Ala Trp Asp Thr Thr Leu Leu Glu Pro Cys Arg Thr Gly Leu
100 105 110

His Gln Gln Leu Asp Asn Leu Asp Ala Cys Leu Gly Gln Val Met Gly
115 120 125

Glu Glu Asp Ser Ala Leu Gly Arg Thr Gly Pro Thr Leu Ala Leu Lys
130 135 140

Arg Tyr Phe Gln Gly Ile His Val Tyr Leu Lys Glu Lys Gly Tyr Ser
145 150 155 160

Asp Cys Ala Trp Glu Thr Val Arg Leu Glu Ile Met Arg Ser Phe Ser
165 170 175

D5 cont

Ser Leu Ile Ser Leu Gln Glu Arg Leu Arg Met Met Asp Gly Asp Leu
180 185 190

Ser Ser Pro
195

<210> 13
<211> 195
<212> PRT
<213> Equus caballus

<400> 13
Met Ala Leu Leu Pro Ser Leu Leu Thr Ala Leu Val Val Tyr Glu Leu
1 5 10 15

Trp Pro Cys Gly Ala Leu Gly Cys Asp Leu Pro Gln Asn His Ile Leu
20 25 30

```
Val Ser Arg Lys Asn Phe Val Leu Leu Gly Gln Met Ser Arg Ile Ser
         35                  40                  45

Ser Ala Ile Cys Leu Lys Asp Arg Lys Asp Phe Arg Phe Pro Gln Asp
     50                  55                  60

Met Ala Asp Gly Arg Gln Phe Pro Glu Ala Gln Ala Ala Ser Val Leu
 65                  70                  75                  80

His Glu Met Leu Gln Gln Ile Phe Ser Leu Phe His Thr Glu Arg Ser
                 85                  90                  95

Ser Ala Ala Trp Asn Thr Thr Leu Leu Asp Glu Leu Cys Thr Gly Leu
            100                 105                 110

Leu Arg Gln Leu Glu Asp Leu Asp Thr Cys Leu Glu Gln Glu Met Gly
        115                 120                 125

Glu Glu Glu Ser Ala Leu Gly Thr Val Arg Pro Thr Leu Ala Val Lys
    130                 135                 140

Arg Tyr Phe Arg Gly Ile His Leu Tyr Leu Lys Glu Lys Lys Tyr Ser
145                 150                 155                 160

Asp Cys Ala Trp Glu Ile Val Arg Met Glu Ile Met Arg Ser Phe Ser
                165                 170                 175

Ser Ser Ala Asn Leu Gln Gly Arg Leu Arg Met Lys Asp Gly Asp Leu
            180                 185                 190

Gly Ser Pro
        195
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<210> 14
<211> 195
<212> PRT
<213> Homo sapiens

D5 Cont

<400> 14

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Met Ala Leu Leu Phe Pro Leu Leu Ala Ala Leu Val Met Thr Ser Tyr
  1               5                  10                  15

Ser Pro Val Gly Ser Leu Gly Cys Asp Leu Pro Gln Asn His Gly Leu
             20                  25                  30

Leu Ser Arg Asn Thr Leu Val Leu Leu His Gln Met Arg Arg Ile Ser
         35                  40                  45

Pro Phe Leu Cys Leu Lys Asp Arg Arg Asp Phe Arg Phe Pro Gln Glu
     50                  55                  60

Met Val Lys Gly Ser Gln Leu Gln Lys Ala His Val Met Ser Val Leu
 65                  70                  75                  80

His Glu Met Leu Gln Gln Ile Phe Ser Leu Phe His Thr Glu Arg Ser
                 85                  90                  95
```

Ser Ala Ala Trp Asn Met Thr Leu Leu Asp Gln Leu His Thr Gly Leu
100 105 110

His Gln Gln Leu Gln His Leu Glu Thr Cys Leu Leu Gln Val Val Gly
115 120 125

Glu Gly Glu Ser Ala Gly Ala Ile Ser Ser Pro Ala Leu Thr Leu Arg
130 135 140

Arg Tyr Phe Gln Gly Ile Arg Val Tyr Leu Lys Glu Lys Lys Tyr Ser
145 150 155 160

Asp Cys Ala Trp Glu Val Val Arg Met Glu Ile Met Lys Ser Leu Phe
165 170 175

Leu Ser Thr Asn Met Gln Glu Arg Leu Arg Ser Lys Asp Arg Asp Leu
180 185 190

Gly Ser Ser
195

<210> 15
<211> 65
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Consensus sequence

<400> 15
Ala Gln Ser Val Leu His Met Gln Gln Ile Phe Leu Phe Thr Glu Ser
1 5 10 15

Ser Ala Ala Trp Asn Thr Leu Leu Thr Gly Leu Gln Leu Leu Cys Gln
20 25 30

D5 Cont

Gly Glu Glu Ser Ala Leu Pro Leu Arg Tyr Phe Gln Gly Tyr Leu Lys
35 40 45

Glu Lys Lys Tyr Ser Cys Ala Trp Glu Val Arg Glu Ile Met Ser Leu
50 55 60

Gln
65

<210> 16
<211> 166
<212> PRT
<213> Homo sapiens

<400> 16
Met Ser Tyr Asn Leu Leu Gly Phe Leu Gln Arg Ser Ser Asn Phe Gln
1 5 10 15

Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg Leu Glu Tyr Cys Leu
20 25 30

Lys Asp Arg Met Asn Phe Asp Ile Pro Glu Glu Ile Lys Gln Leu Gln
35 40 45

Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr Ile Tyr Glu Met Leu Gln
50 55 60

Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser Ser Thr Gly Trp Asn
65 70 75 80

Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val Tyr His Gln Ile Asn
85 90 95

His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu Lys Glu Asp Phe Thr
100 105 110

Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys Arg Tyr Tyr Gly Arg
115 120 125

Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser His Cys Ala Trp Thr
130 135 140

Ile Val Arg Val Glu Ile Leu Arg Asn Phe Tyr Phe Ile Asn Arg Leu
145 150 155 160

Thr Gly Tyr Leu Arg Asn
165

<210> 17
<211> 165
<212> PRT
<213> Homo sapiens

<400> 17
Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg Arg Thr Leu Met
1 5 10 15

Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp
20 25 30

Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln
35 40 45

Lys Ala Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe
50 55 60

Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu
65 70 75 80

Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu Glu
85 90 95

Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met Asn

```
            100                 105                 110

Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr Leu
        115                 120                 125

Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val Arg
    130                 135                 140

Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu Ser
145                 150                 155                 160

Leu Arg Ser Lys Glu
                165
```

<210> 18
<211> 189
<212> PRT
<213> Mus musculus

<400> 18

```
Met Ala Arg Leu Cys Ala Phe Leu Met Val Leu Ala Val Met Ser Tyr
  1               5                  10                  15

Trp Pro Thr Cys Ser Leu Gly Cys Asp Leu Pro Gln Thr His Asn Leu
             20                  25                  30

Arg Asn Lys Arg Ala Leu Thr Leu Leu Val Gln Met Arg Arg Leu Ser
         35                  40                  45

Pro Leu Ser Cys Leu Lys Asp Arg Lys Asp Phe Gly Phe Pro Gln Glu
     50                  55                  60

Lys Val Asp Ala Gln Gln Ile Lys Lys Ala Gln Ala Ile Pro Val Leu
 65                  70                  75                  80

Ser Glu Leu Thr Gln Gln Ile Leu Asn Ile Phe Thr Ser Lys Asp Ser
                 85                  90                  95

Ser Ala Ala Trp Asn Ala Thr Leu Leu Asp Ser Phe Cys Asn Asp Leu
            100                 105                 110

His Gln Gln Leu Asn Asp Leu Gln Gly Cys Leu Met Gln Gln Val Gly
        115                 120                 125

Val Gln Glu Phe Pro Leu Thr Gln Glu Asp Ala Leu Leu Ala Val Arg
    130                 135                 140

Lys Tyr Phe His Arg Ile Thr Val Tyr Leu Arg Glu Lys Lys His Ser
145                 150                 155                 160

Pro Cys Ala Trp Glu Val Val Arg Ala Glu Val Trp Arg Ala Leu Ser
                165                 170                 175

Ser Ser Ala Asn Val Leu Gly Arg Leu Arg Glu Glu Lys
            180                 185
```

D5 Cont

<210> 19
<211> 195
<212> PRT
<213> Antilocapra americana

<400> 19
Met Ala Gln Leu Leu Pro Leu Leu Thr Ala Leu Val Leu Cys Ser Tyr
1 5 10 15

Gly Pro Val Gly Ser Leu Gly Cys Asp Leu Pro His Asn Ser Ala Pro
20 25 30

Leu Ser Arg Lys Thr Leu Val Leu Leu Asp Gln Met Arg Arg Val Ser
35 40 45

Pro Val Leu Cys Leu Lys Asp Arg Arg Asp Phe Gln Phe Pro Arg Glu
50 55 60

Val Val Asn Gly Ser Gln Phe Gln Lys Asn Gln Thr Val Ser Val Leu
65 70 75 80

His Glu Met Leu Gln Gln Ile Phe Asn Leu Leu His Thr Ala Arg Ser
85 90 95

Ser Ala Ala Trp Asn Asn Thr Leu Leu Glu Glu Leu His Thr Ala Leu
100 105 110

His Gln Gln Leu Gln Gly Leu Glu Thr Cys Leu Val Gln Ala Met Gly
115 120 125

Glu Glu Asp Ser Val Leu Thr Ala Asp Ser Pro Met Leu Met Leu Lys
130 135 140

Arg Tyr Phe Gln Arg Ile Arg Leu Tyr Leu Asp Glu Lys Lys His Ser
145 150 155 160

Gly Cys Ala Trp Glu Leu Val Arg Met Glu Ile Arg Arg Ala Phe Ser
165 170 175

Ser Thr Ala Asp Leu Gln Glu Ser Leu Arg Ser Lys Asp Gly Asp Leu
180 185 190

Ala Ser Ser
195

D5 cont

<210> 20
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Consensus sequence

<400> 20

```
Phe Pro Glu Gln Lys Leu Glu Met Gln Gln Ile Phe Phe Ser Ser Ala
  1               5                  10                  15

Trp Asn Thr Leu Gln Gln Leu Leu Cys Gly Leu Leu Tyr Phe Arg Ile
             20                  25                  30

Tyr Leu Glu Lys Lys Ser Cys Ala Trp Glu Val
         35                  40
```

<210> 21
<211> 184
<212> PRT
<213> Equus caballus

<400> 21

```
Met Ala Leu Pro Val Ser Leu Leu Met Ala Leu Val Val Leu Ser Cys
  1               5                  10                  15

His Ser Ile Cys Ser Leu Gly Cys Asp Leu Pro His Thr His Ser Leu
             20                  25                  30

Gly Asn Thr Arg Val Leu Met Leu Leu Gly Gln Met Arg Arg Ile Ser
         35                  40                  45

Pro Phe Ser Cys Leu Lys Asp Arg Asn Asp Phe Gly Phe Pro Gln Glu
     50                  55                  60

Val Phe Asp Gly Asn Gln Phe Arg Lys Pro Gln Ala Ile Ser Ala Val
 65                  70                  75                  80

His Glu Thr Ile Gln Gln Ile Phe His Leu Phe Ser Thr Asp Gly Ser
                 85                  90                  95

Ser Ala Ala Trp Asp Glu Ser Leu Leu Asp Lys Leu Tyr Thr Gly Leu
            100                 105                 110

Tyr Gln Gln Leu Thr Glu Leu Glu Ala Cys Leu Ser Gln Glu Val Gly
        115                 120                 125

Val Glu Glu Thr Pro Leu Met Asn Glu Asp Ser Leu Leu Ala Val Arg
    130                 135                 140

Arg Tyr Phe Gln Arg Ile Ala Leu Tyr Leu Gln Glu Lys Lys Tyr Ser
145                 150                 155                 160

Pro Cys Ala Trp Glu Ile Val Arg Ala Glu Ile Met Arg Ser Phe Ser
                165                 170                 175

Ser Ser Thr Asn Leu Pro Gln Ser
            180
```

<210> 22
<211> 92
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Consensus sequence

<400> 22
Ser Leu Leu Ala Leu Val Ser Leu Gly Cys Asp Leu Pro His Leu Leu
1 5 10 15

Leu Gln Met Arg Cys Lys Asp Arg Asp Phe Phe Pro Gln Gly Gln Lys
20 25 30

Ala Gln Ser His Gln Gln Ile Phe Leu Phe Thr Ser Ser Ala Ala Trp
35 40 45

Asn Leu Leu Asp Leu Thr Gly Leu Gln Leu Leu Glu Cys Gln Glu Gly
50 55 60

Glu Leu Leu Arg Tyr Phe Gln Tyr Leu Glu Lys Lys Tyr Ser Cys Ala
65 70 75 80

Trp Glu Val Arg Glu Ile Met Ser Ser Thr Leu Gln
85 90

<210> 23
<211> 3144
<212> DNA
<213> Homo sapiens

<400> 23
gcctggctcc ctctcgctga gacacacata cactcacaca tacacaaccc ggcaggctcg 60
tctgaacttg aagacacccc acattccaag atgcccgagg ttcctgggaa tgcctggggt 120
tcttcgatcc ggaaaatcct accggcatcc tcctagggag ggattattat tattattttt 180
ctttaatctg gaagagaaga gaacaagttg tgcttttccc cccttcttct tgctaaacgc 240
catggatata actgaataag cggctcaggg ctttccccgc gtggacgtcc gaggccacca 300
tctgcctgca ttcgccggag ccgccggagg gtttagctcg agtctgtctc gggcggggaa 360
ggatgcgtgg ccgagccggg gagcccgggc gccccgcgga gccggcctcg gtgccaccca 420
gccgggggta gatgctgcct cgcccaggcg ctgagtgacc agaccatgga gaccctgctt 480
ggtggcctgc tagcgtttgg catggcgttt gccgtggtcg acgcctgccc caagtactgt 540
gtctgccaga atctgtctga gtcactgggg accctgtgcc cctccaaggg gctgctcttt 600
gtaccccctg atattgaccg gcggacagtg gagctgcgcc tgggcggcaa cttcatcatc 660
cacatcagcc gccaggactt tgccaacatg acggggctgg tggacctgac cctgtccagg 720
aacaccatca gccacatcca gccctttttcc tttctggacc tcgagagcct ccgctccctg 780
catcttgaca gcaatcggct gccaagcctt ggggaggaca ccctccgggg cctggtcaac 840
ctgcagcacc ttatcgtgaa caacaaccag ctgggcggca tcgcagatga ggcttttgag 900
gacttcctgc tgacattgga ggatctggac ctctcctaca acaacctcca tggcctgccg 960
tgggactccg tgcgacgcat ggtcaacctc caccagctga gcctggacca caacctgctg 1020
gatcacatcg ccgagggcac ctttgcagac ctgcagaaac tggcccgcct ggatctcacc 1080
tccaatcggc tgcagaagct gccccctgat cccatctttg cccgctccca ggcttcggct 1140
ttgacagcca cacccttgc cccacccttg tcctttagtt ttgggggtaa cccacttcac 1200
tgcaattgtg agcttctctg gctgcggagg ctcgagcggg acgatgacct ggaaacctgt 1260
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tgcgagccgc ctctcatcac ccagcacaca cacaagttgc tggttctgga gggccaggcg 1380
gccacactca agtgcaaagc cattggggac cccagccccc ttatccactg ggtagccccc 1440
gatgaccgcc tggtagggaa ctcctcaagg accgctgtct atgacaatgg caccctggac 1500
atcttcatca ccacatctca ggacagtggt gccttcacct gcattgctgc caatgctgcc 1560
ggagaggcca cggccatggt ggaggtctcc atcgtccagc tgccacacct cagcaacagc 1620

```
accagccgca ctgcaccccc caagtcccgc ctctcagaca tcactggctc cagcaagacc 1680
agccggggag gtggaggcag tgggggcgga gagcctccca aaagcccccc ggaacgggct 1740
gtgcttgtgt ctgaagtgac caccacctcg gccctggtca agtggtctgt cagcaagtca 1800
gcaccccggg tgaagatgta ccagctgcag tacaactgct ctgacgatga ggtactgatt 1860
tacaggatga tcccagcctc caacaaggcc ttcgtggtca acaacctggt gtcagggact 1920
ggctacgact tgtgtgtgct ggccatgtgg gatgacacag ccacgacact cacggccacc 1980
aacatcgtgg gctgcgccca gttcttcacc aaggctgact acccgcagtg ccagtccatg 2040
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ctgctggtct tcatcgtcat cctcatggtg cgctacaagg tctgcaacca cgaggccccc 2160
agcaagatgg cagcggccgt gagcaatgtg tactcgcaga ccaacggcgc ccagccaccg 2220
cctccaagca gcgcaccagc cggggccccg ccgcagggcc cgccgaaggt ggtggtgcgc 2280
aacgagctcc tggacttcac cgccagcctg gcccgcgcca gtgactcctc ttcctccagc 2340
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gccccgcgcc ccaagcccag ccttgaccgc ctgatggggg ccttcgcctc cctggacctc 2460
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gccaggagcc tgctcccctt gccgttggag ggcaaggcca aacgcagcca ctccttcgac 2640
atgggggact ttgctgctgc ggcggcggga ggggtcgtgc cgggcggcta cagtcctcct 2700
cggaaggtct cgaacatctg gacgaagcgc agcctctctg tcaacggcat gctcttgccc 2760
tttgaggaga gtgacctggt gggggcccgg gggacttttg gcagctccga atgggtgatg 2820
gagagcacgg tctaggtggg ggtgggcatg ctccctttcc tgtgcgcagg gtgggagaag 2880
gggaaagaat ctcactggca agtgtttgtg gagtttccat ggtgatgttt acatccaggg 2940
acagtttcgt ctccctgtca atggcctcgt gtcccccccc accccgcaac acccacatca 3000
cctccccacc acccggccgg ggtgtgctca gggaatgtgg actcgctcaa atgccggact 3060
gagccctgag tgtttggaaa ggcgagactc cgcctttcta atcacaaatg tagcctacaa 3120
gcaagcggct ttggattgct tatg                                       3144
```

<210> 24
<211> 832
<212> PRT
<213> Homo sapiens

<400> 24

```
Leu Glu Ser Val Ser Gly Gly Glu Gly Cys Val Ala Glu Pro Gly Ser
  1               5                  10                  15

Pro Gly Ala Pro Arg Ser Arg Pro Arg Cys His Pro Ala Gly Gly Arg
             20                  25                  30

Cys Cys Leu Ala Gln Ala Leu Ser Asp Gln Thr Met Glu Thr Leu Leu
         35                  40                  45

Gly Gly Leu Leu Ala Phe Gly Met Ala Phe Ala Val Val Asp Ala Cys
     50                  55                  60

Pro Lys Tyr Cys Val Cys Gln Asn Leu Ser Glu Ser Leu Gly Thr Leu
 65                  70                  75                  80

Cys Pro Ser Lys Gly Leu Leu Phe Val Pro Pro Asp Ile Asp Arg Arg
                 85                  90                  95

Thr Val Glu Leu Arg Leu Gly Gly Asn Phe Ile Ile His Ile Ser Arg
            100                 105                 110

Gln Asp Phe Ala Asn Met Thr Gly Leu Val Asp Leu Thr Leu Ser Arg
        115                 120                 125
```

D5 cont

```
Asn Thr Ile Ser His Ile Gln Pro Phe Ser Phe Leu Asp Leu Glu Ser
    130                 135                 140

Leu Arg Ser Leu His Leu Asp Ser Asn Arg Leu Pro Ser Leu Gly Glu
145                 150                 155                 160

Asp Thr Leu Arg Gly Leu Val Asn Leu Gln His Leu Ile Val Asn Asn
                165                 170                 175

Asn Gln Leu Gly Gly Ile Ala Asp Glu Ala Phe Glu Asp Phe Leu Leu
            180                 185                 190

Thr Leu Glu Asp Leu Asp Leu Ser Tyr Asn Asn Leu His Gly Leu Pro
        195                 200                 205

Trp Asp Ser Val Arg Arg Met Val Asn Leu His Gln Leu Ser Leu Asp
    210                 215                 220

His Asn Leu Leu Asp His Ile Ala Glu Gly Thr Phe Ala Asp Leu Gln
225                 230                 235                 240

Lys Leu Ala Arg Leu Asp Leu Thr Ser Asn Arg Leu Gln Lys Leu Pro
                245                 250                 255

Pro Asp Pro Ile Phe Ala Arg Ser Gln Ala Ser Ala Leu Thr Ala Thr
            260                 265                 270

Pro Phe Ala Pro Pro Leu Ser Phe Ser Phe Gly Gly Asn Pro Leu His
        275                 280                 285

Cys Asn Cys Glu Leu Leu Trp Leu Arg Arg Leu Glu Arg Asp Asp Asp
    290                 295                 300

Leu Glu Thr Cys Gly Ser Pro Gly Gly Leu Lys Gly Arg Tyr Phe Trp
305                 310                 315                 320

His Val Arg Glu Glu Glu Phe Val Cys Glu Pro Pro Leu Ile Thr Gln
                325                 330                 335

His Thr His Lys Leu Leu Val Leu Glu Gly Gln Ala Ala Thr Leu Lys
            340                 345                 350

Cys Lys Ala Ile Gly Asp Pro Ser Pro Leu Ile His Trp Val Ala Pro
        355                 360                 365

Asp Asp Arg Leu Val Gly Asn Ser Ser Arg Thr Ala Val Tyr Asp Asn
    370                 375                 380

Gly Thr Leu Asp Ile Phe Ile Thr Thr Ser Gln Asp Ser Gly Ala Phe
385                 390                 395                 400

Thr Cys Ile Ala Ala Asn Ala Ala Gly Glu Ala Thr Ala Met Val Glu
                405                 410                 415

Val Ser Ile Val Gln Leu Pro His Leu Ser Asn Ser Thr Ser Arg Thr
            420                 425                 430
```

D5 cont

```
Ala Pro Pro Lys Ser Arg Leu Ser Asp Ile Thr Gly Ser Ser Lys Thr
        435                 440                 445

Ser Arg Gly Gly Gly Gly Ser Gly Gly Gly Glu Pro Pro Lys Ser Pro
    450                 455                 460

Pro Glu Arg Ala Val Leu Val Ser Glu Val Thr Thr Thr Ser Ala Leu
465                 470                 475                 480

Val Lys Trp Ser Val Ser Lys Ser Ala Pro Arg Val Lys Met Tyr Gln
                485                 490                 495

Leu Gln Tyr Asn Cys Ser Asp Asp Glu Val Leu Ile Tyr Arg Met Ile
            500                 505                 510

Pro Ala Ser Asn Lys Ala Phe Val Val Asn Asn Leu Val Ser Gly Thr
        515                 520                 525

Gly Tyr Asp Leu Cys Val Leu Ala Met Trp Asp Asp Thr Ala Thr Thr
    530                 535                 540

Leu Thr Ala Thr Asn Ile Val Gly Cys Ala Gln Phe Phe Thr Lys Ala
545                 550                 555                 560

Asp Tyr Pro Gln Cys Gln Ser Met His Ser Gln Ile Leu Gly Gly Thr
                565                 570                 575

Met Ile Leu Val Ile Gly Gly Ile Ile Val Ala Thr Leu Leu Val Phe
            580                 585                 590

Ile Val Ile Leu Met Val Arg Tyr Lys Val Cys Asn His Glu Ala Pro
        595                 600                 605

Ser Lys Met Ala Ala Ala Val Ser Asn Val Tyr Ser Gln Thr Asn Gly
    610                 615                 620

Ala Gln Pro Pro Pro Pro Ser Ser Ala Pro Ala Gly Ala Pro Pro Gln
625                 630                 635                 640

Gly Pro Pro Lys Val Val Val Arg Asn Glu Leu Leu Asp Phe Thr Ala
                645                 650                 655

Ser Leu Ala Arg Ala Ser Asp Ser Ser Ser Ser Ser Ser Leu Gly Ser
            660                 665                 670

Gly Glu Ala Ala Gly Leu Gly Arg Ala Pro Trp Arg Ile Pro Pro Ser
        675                 680                 685

Ala Pro Arg Pro Lys Pro Ser Leu Asp Arg Leu Met Gly Ala Phe Ala
    690                 695                 700

Ser Leu Asp Leu Lys Ser Gln Arg Lys Glu Glu Leu Leu Asp Ser Arg
705                 710                 715                 720

Thr Pro Ala Gly Arg Gly Ala Gly Thr Ser Ala Arg Gly His His Ser
                725                 730                 735
```

D5 Cont

```
Asp Arg Glu Pro Leu Leu Gly Pro Pro Ala Ala Arg Ala Arg Ser Leu
            740                 745                 750

Leu Pro Leu Pro Leu Glu Gly Lys Ala Lys Arg Ser His Ser Phe Asp
        755                 760                 765

Met Gly Asp Phe Ala Ala Ala Ala Ala Gly Gly Val Val Pro Gly Gly
    770                 775                 780

Tyr Ser Pro Pro Arg Lys Val Ser Asn Ile Trp Thr Lys Arg Ser Leu
785                 790                 795                 800

Ser Val Asn Gly Met Leu Leu Pro Phe Glu Glu Ser Asp Leu Val Gly
                805                 810                 815

Ala Arg Gly Thr Phe Gly Ser Ser Glu Trp Val Met Glu Ser Thr Val
            820                 825                 830
```

<210> 25
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:IFAbd Domain
13-110

<400> 25

```
Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr Ile Tyr Glu Met Leu Gln
  1               5                  10                  15

Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser Ser Thr Gly Trp Asn
             20                  25                  30

Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val Tyr His Gln Ile Asn
         35                  40                  45

His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu Lys Glu Asp Phe Thr
     50                  55                  60

Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys Arg Tyr Tyr Gly Arg
 65                  70                  75                  80

Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser His Cys Ala Trp Thr
                 85                  90                  95

Ile Val
```

<210> 26
<211> 183

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:pfam00143
Domain 5-187

<400> 26
Ser Ser Phe Leu Val Ala Leu Val Ala Leu Gly Cys Asn Ser Val Cys
1 5 10 15

Ser Leu Gly Cys Asp Leu Pro Gln Thr His Gly Leu Leu Asn Arg Arg
20 25 30

Ala Leu Thr Leu Leu Gly Gln Met Arg Arg Leu Pro Ala Ser Ser Cys
35 40 45

Gln Lys Asp Arg Asn Asp Phe Ala Phe Pro Gln Asp Val Phe Gly Gly
50 55 60

Asp Gln Ser His Lys Ala Gln Ala Leu Ser Val Val His Val Thr Asn
65 70 75 80

Gln Lys Ile Phe His Phe Phe Cys Thr Glu Ala Ser Ser Ser Ala Ala
85 90 95

Trp Asn Thr Thr Leu Leu Glu Glu Phe Cys Thr Gly Leu Asp Arg Gln
100 105 110

Leu Thr Arg Leu Glu Ala Cys Val Leu Gln Glu Val Glu Glu Gly Glu
115 120 125

Ala Pro Leu Thr Asn Glu Asp Ile His Pro Glu Asp Ser Ile Leu Arg
130 135 140

Asn Tyr Phe Gln Arg Leu Ser Leu Tyr Leu Gln Glu Lys Lys Tyr Ser
145 150 155 160

Pro Cys Ala Trp Glu Ile Val Arg Ala Glu Ile Met Arg Ser Leu Tyr
165 170 175

Tyr Ser Ser Thr Ala Leu Gln
180

D5 Cont

<210> 27
<211> 786
<212> PRT
<213> Homo sapiens

<400> 27
Met Glu Thr Leu Leu Gly Gly Leu Leu Ala Phe Gly Met Ala Phe Ala
1 5 10 15

Val Val Asp Ala Cys Pro Lys Tyr Cys Val Cys Gln Asn Leu Ser Glu
20 25 30

```
Ser Leu Gly Thr Leu Cys Pro Ser Lys Gly Leu Leu Phe Val Pro Pro
         35                  40                  45

Asp Ile Asp Arg Arg Thr Val Glu Leu Arg Leu Gly Gly Asn Phe Ile
     50                  55                  60

Ile His Ile Ser Arg Gln Asp Phe Ala Asn Met Thr Gly Leu Val Asp
 65                  70                  75                  80

Leu Thr Leu Ser Arg Asn Thr Ile Ser His Ile Gln Pro Phe Ser Phe
                 85                  90                  95

Leu Asp Leu Glu Ser Leu Arg Ser Leu His Leu Asp Ser Asn Arg Leu
            100                 105                 110

Pro Ser Leu Gly Glu Asp Thr Leu Arg Gly Leu Val Asn Leu Gln His
        115                 120                 125

Leu Ile Val Asn Asn Asn Gln Leu Gly Gly Ile Ala Asp Glu Ala Phe
    130                 135                 140

Glu Asp Phe Leu Leu Thr Leu Glu Asp Leu Asp Leu Ser Tyr Asn Asn
145                 150                 155                 160

Leu His Gly Leu Pro Trp Asp Ser Val Arg Arg Met Val Asn Leu His
                165                 170                 175

Gln Leu Ser Leu Asp His Asn Leu Leu Asp His Ile Ala Glu Gly Thr
            180                 185                 190

Phe Ala Asp Leu Gln Lys Leu Ala Arg Leu Asp Leu Thr Ser Asn Arg
        195                 200                 205

Leu Gln Lys Leu Pro Pro Asp Pro Ile Phe Ala Arg Ser Gln Ala Ser
    210                 215                 220

Ala Leu Thr Ala Thr Pro Phe Ala Pro Pro Leu Ser Phe Ser Phe Gly
225                 230                 235                 240

Gly Asn Pro Leu His Cys Asn Cys Glu Leu Leu Trp Leu Arg Arg Leu
                245                 250                 255

Glu Arg Asp Asp Asp Leu Glu Thr Cys Gly Ser Pro Gly Gly Leu Lys
            260                 265                 270

Gly Arg Tyr Phe Trp His Val Arg Glu Glu Glu Phe Val Cys Glu Pro
        275                 280                 285

Pro Leu Ile Thr Gln His Thr His Lys Leu Leu Val Leu Glu Gly Gln
    290                 295                 300

Ala Ala Thr Leu Lys Cys Lys Ala Ile Gly Asp Pro Ser Pro Leu Ile
305                 310                 315                 320

His Trp Val Ala Pro Asp Asp Arg Leu Val Gly Asn Ser Ser Arg Thr
                325                 330                 335
```

D5 Cont

```
Ala Val Tyr Asp Asn Gly Thr Leu Asp Ile Phe Ile Thr Thr Ser Gln
            340                 345                 350

Asp Ser Gly Ala Phe Thr Cys Ile Ala Ala Asn Ala Ala Gly Glu Ala
        355                 360                 365

Thr Ala Met Val Glu Val Ser Ile Val Gln Leu Pro His Leu Ser Asn
    370                 375                 380

Ser Thr Ser Arg Thr Ala Pro Pro Lys Ser Arg Leu Ser Asp Ile Thr
385                 390                 395                 400

Gly Ser Ser Lys Thr Ser Arg Gly Gly Gly Gly Ser Gly Gly Gly Glu
                405                 410                 415

Pro Pro Lys Ser Pro Pro Glu Arg Ala Val Leu Val Ser Glu Val Thr
            420                 425                 430

Thr Thr Ser Ala Leu Val Lys Trp Ser Ser Val Ser Lys Ser Ala Pro
        435                 440                 445

Arg Val Lys Met Tyr Gln Leu Gln Tyr Asn Cys Ser Asp Glu Val Leu
    450                 455                 460

Ile Tyr Arg Met Ile Pro Ala Ser Asn Lys Ala Phe Val Val Asn Asn
465                 470                 475                 480

Leu Val Ser Gly Thr Gly Tyr Asp Leu Cys Val Leu Ala Met Trp Asp
                485                 490                 495

Asp Thr Ala Thr Thr Leu Thr Ala Thr Asn Ile Val Gly Cys Ala Gln
            500                 505                 510

Phe Phe Thr Lys Ala Asp Tyr Pro Gln Cys Gln Ser Met His Ser Gln
        515                 520                 525

Ile Leu Gly Gly Thr Met Ile Leu Val Ile Gly Gly Ile Val Ala Thr
    530                 535                 540

Leu Leu Val Phe Ile Val Ile Leu Met Val Arg Tyr Lys Val Cys Asn
545                 550                 555                 560

His Glu Ala Pro Ser Lys Met Ala Ala Ala Val Ser Asn Val Tyr Ser
                565                 570                 575

Gln Thr Asn Gly Ala Gln Pro Pro Pro Ser Ser Ala Pro Ala Gly Ala
            580                 585                 590

Pro Pro Gln Gly Pro Pro Lys Val Val Val Arg Asn Glu Leu Leu Asp
        595                 600                 605

Phe Thr Ala Ser Leu Ala Arg Ala Ser Asp Ser Ser Ser Ser Ser Ser
    610                 615                 620

Leu Gly Ser Gly Glu Ala Ala Gly Leu Gly Arg Ala Trp Arg Ile Pro
625                 630                 635                 640
```

D5 Cont

```
Pro Ser Ala Pro Arg Pro Lys Pro Ser Leu Asp Arg Leu Met Gly Ala
                645                 650                 655

Phe Ala Ser Leu Asp Leu Lys Ser Gln Arg Lys Glu Glu Leu Leu Asp
            660                 665                 670

Ser Arg Thr Pro Ala Gly Arg Gly Ala Gly Thr Ser Ala Arg Gly His
        675                 680                 685

His Ser Asp Arg Glu Pro Leu Leu Gly Pro Pro Ala Ala Arg Ala Arg
    690                 695                 700

Ser Leu Leu Pro Leu Pro Leu Glu Gly Lys Ala Lys Arg Ser His Ser
705                 710                 715                 720

Phe Asp Met Gly Asp Phe Ala Ala Ala Ala Ala Gly Gly Val Val Pro
                725                 730                 735

Gly Gly Tyr Ser Pro Pro Arg Lys Val Ser Asn Ile Trp Thr Lys Arg
            740                 745                 750

Ser Leu Ser Val Asn Gly Met Leu Leu Pro Phe Glu Glu Ser Asp Leu
        755                 760                 765

Val Gly Ala Arg Gly Thr Phe Gly Ser Ser Glu Trp Val Met Glu Ser
    770                 775                 780

Thr Val
785
```